



PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/831,233A

DATE: 06/12/2002

TIME: 14:14:10

Input Set : A:\BB1129 us pct seq 1st.txt

Output Set: N:\CRF3\06122002\I831233A.raw

p.6

3 <110> APPLICANT: E. I. du Pont de Nemours and Company
 5 <120> TITLE OF INVENTION: Plant Glutamine Amidotransferase Homologs
 7 <130> FILE REFERENCE: BB1129
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/831,233A
 C--> 10 <141> CURRENT FILING DATE: 2001-09-14
 12 <150> PRIOR APPLICATION NUMBER: 60/107,275
 13 <151> PRIOR FILING DATE: 1998-11-05
 15 <160> NUMBER OF SEQ ID NOS: 15
 17 <170> SOFTWARE: Microsoft Office 97
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 1956
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Impatiens balsamia
 24 <400> SEQUENCE: 1

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26	ggctggtgca	ggcggagatt	ctgtggtgac	tttacttgat	tacggtgctg	gaaatgttag	120
27	gagtgtgagg	aacgccatcc	gcacacttgg	atttgatata	aaagatgtgc	aaaagccaga	180
28	ggatattcta	aattgctaagc	gccttatctt	tcctggcggt	ggggcctttg	cacctgcaat	240
29	ggatgttctt	attcgtaaag	ggctggctga	agcactctgt	acttacattc	agaatgatcg	300
30	acctttcctg	ggtatatgcc	tgggattgca	gctactcttt	gagtcaagtg	aagaaaatgg	360
31	tccaattcaa	ggtcttggct	tgattcctgg	acgggttggg	cgttttgaa	catccaatgg	420
32	tttaaggggtg	ccacatattg	gatggcatgc	cttgatata	aaggaagggg	cagcaatttt	480
33	agatgatgtg	gggaatcaac	atgtgtatit	tgttcaactca	tatcgagcca	atgccgagga	540
34	caacaaagag	tggatttcat	ctacatgcag	ctatggtgac	gattttattg	catccatttca	600
35	gaagggaagt	gttcatgcag	tccaatttca	tcccagagaag	agtggagggtg	ttggaatttcc	660
36	catattgaga	agatttttga	atgctgattc	ctttaacaac	aaaagacaga	agccaatgaa	720
37	tggaaaggct	tctaaacttg	caaagagagt	aattgcttgc	cttgatgtga	gggcaaatga	780
38	taatggggat	cttgttgtaa	ccaagggaga	ccaatatgat	gtgagagaac	gtacagaaga	840
39	gaatgagggtc	agaaaccttg	gcaagcctgt	tgaacttget	gggcagtatt	atttagacgg	900
40	tgctgatgag	gtcagcttct	taaacattac	tggtttccgg	gacttccctc	taggcgatct	960
41	acccatgcta	caggtcttgc	aacgcgcata	tgaaaacgtt	tttgtgccat	taactgtcgg	1020
42	gggtggcatc	agggatttta	ctgatgcaaa	tgggaaggat	tattctagtc	tagaagtggc	1080
43	ttcagagtat	ttcagatcgg	gcgccgataa	ggtttcgatc	ggaagtgatg	cagtttacac	1140
44	tgctgaggaa	tatatataaa	ccggagtgaa	gacaggaaaag	agcagcatag	agcagatatc	1200
45	tacagtatat	ggtaaccagg	cagtggttgt	aagcattgat	cctcgccgag	tttacttgag	1260
46	aaaacccgat	gaagtagaat	ttaaagccat	caaagtaagc	catccagggtc	caaacggtga	1320
47	ggaatatgcc	tggtatcagt	gcaactgtta	tggtggacga	gaagggagac	ccatcggagc	1380
48	ttatgaacta	gctaaggctg	ttgaggaact	tggagctgga	gaaatattat	tgaactgcat	1440
49	tgattgtgat	ggtcaaggaa	aaggattcga	tatagatctg	atcaagctaa	tatccgatgc	1500
50	tgtgaacatt	cctgttatcg	caagcagcgg	tgcaggagtc	gctgatoact	tctccgaagt	1560
51	ctttaatgaa	accaacgcac	ctgctgccct	tgcagctggc	attttccatc	gcaaagaggt	1620
52	tccaattaag	gctgtttaaag	agcacttggt	gaaggaaggg	attgaagtta	gattgtaagg	1680
53	cgagaatcac	ttggaagaaa	tttcatcttg	aagttcaatt	ttgttacaca	agagatttcc	1740

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54 ttctttcttg gcctatgtga tatttattta tttatgtttt gctattgaat tattgttatt 1800
55 attatttttg catttggtat ttgaatagat ttgagttttt agaccttggt gtgtcctggt 1860
56 tatctctagg ccatgttttg tggattatat acaagtgtga aattaaataa ataaatcgta 1920
57 tgaatttatg cttttaaaaa aaaaaaaaaa aaaaaa 1956
59 <210> SEQ ID NO: 2
60 <211> LENGTH: 558
61 <212> TYPE: PRT
62 <213> ORGANISM: Impatiens balsamia
64 <400> SEQUENCE: 2
65 His Glu Lys Glu Leu Ala Ser Thr Lys Pro Gln Asn Gly Phe Arg Ile
66 1 5 10 15
68 Arg Ala Ala Leu Ala Gly Ala Gly Gly Asp Ser Val Val Thr Leu Leu
69 20 25 30
71 Asp Tyr Gly Ala Gly Asn Val Arg Ser Val Arg Asn Ala Ile Arg Thr
72 35 40 45
74 Leu Gly Phe Asp Ile Lys Asp Val Gln Lys Pro Glu Asp Ile Leu Asn
75 50 55 60
77 Ala Lys Arg Leu Ile Phe Pro Gly Val Gly Ala Phe Ala Pro Ala Met
78 65 70 75 80
80 Asp Val Leu Ile Arg Lys Gly Leu Ala Glu Ala Leu Cys Thr Tyr Ile
81 85 90 95
83 Gln Asn Asp Arg Pro Phe Leu Gly Ile Cys Leu Gly Leu Gln Leu Leu
84 100 105 110
86 Phe Glu Ser Ser Glu Glu Asn Gly Pro Ile Gln Gly Leu Gly Leu Ile
87 115 120 125
89 Pro Gly Arg Val Gly Arg Phe Glu Ser Ser Asn Gly Leu Arg Val Pro
90 130 135 140
92 His Ile Gly Trp His Ala Leu Asp Ile Lys Glu Gly Ser Ala Ile Leu
93 145 150 155 160
95 Asp Asp Val Gly Asn Gln His Val Tyr Phe Val His Ser Tyr Arg Ala
96 165 170 175
98 Asn Ala Glu Asp Asn Lys Glu Trp Ile Ser Ser Thr Cys Ser Tyr Gly
99 180 185 190
101 Asp Asp Phe Ile Ala Ser Ile Gln Lys Gly Asn Val His Ala Val Gln
102 195 200 205
104 Phe His Pro Glu Lys Ser Gly Gly Val Gly Leu Ser Ile Leu Arg Arg
105 210 215 220
107 Phe Leu Asn Ala Asp Ser Phe Asn Asn Lys Arg Gln Lys Pro Met Asn
108 225 230 235 240
110 Gly Lys Ala Ser Lys Leu Ala Lys Arg Val Ile Ala Cys Leu Asp Val
111 245 250 255
113 Arg Ala Asn Asp Asn Gly Asp Leu Val Val Thr Lys Gly Asp Gln Tyr
114 260 265 270
116 Asp Val Arg Glu Arg Thr Glu Glu Asn Glu Val Arg Asn Leu Gly Lys
117 275 280 285
119 Pro Val Glu Leu Ala Gly Gln Tyr Tyr Leu Asp Gly Ala Asp Glu Val
120 290 295 300
122 Ser Phe Leu Asn Ile Thr Gly Phe Arg Asp Phe Pro Leu Gly Asp Leu
123 305 310 315 320

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125 Pro Met Leu Gln Val Leu Gln Arg Ala Ser Glu Asn Val Phe Val Pro
126                               325                               330                               335
128 Leu Thr Val Gly Gly Ile Arg Asp Phe Thr Asp Ala Asn Gly Arg
129                               340                               345                               350
131 Tyr Tyr Ser Ser Leu Glu Val Ala Ser Glu Tyr Phe Arg Ser Gly Ala
132                               355                               360                               365
134 Asp Lys Val Ser Ile Gly Ser Asp Ala Val Tyr Thr Ala Glu Glu Tyr
135                               370                               375                               380
137 Ile Lys Thr Gly Val Lys Thr Gly Lys Ser Ser Ile Glu Gln Ile Ser
138 385                               390                               395                               400
140 Thr Val Tyr Gly Asn Gln Ala Val Val Val Ser Ile Asp Pro Arg Arg
141                               405                               410                               415
143 Val Tyr Leu Arg Lys Pro Asp Glu Val Glu Phe Lys Ala Ile Lys Val
144                               420                               425                               430
146 Ser His Pro Gly Pro Asn Gly Glu Glu Tyr Ala Trp Tyr Gln Cys Thr
147                               435                               440                               445
149 Val Asn Gly Gly Arg Glu Gly Arg Pro Ile Gly Ala Tyr Glu Leu Ala
150                               450                               455                               460
152 Lys Ala Val Glu Glu Leu Gly Ala Gly Glu Ile Leu Leu Asn Cys Ile
153 465                               470                               475                               480
155 Asp Cys Asp Gly Gln Gly Lys Gly Phe Asp Ile Asp Leu Ile Lys Leu
156                               485                               490                               495
158 Ile Ser Asp Ala Val Asn Ile Pro Val Ile Ala Ser Ser Gly Ala Gly
159                               500                               505                               510
161 Val Ala Asp His Phe Ser Glu Val Phe Asn Glu Thr Asn Ala Ser Ala
162                               515                               520                               525
164 Ala Leu Ala Ala Gly Ile Phe His Arg Lys Glu Val Pro Ile Lys Ala
165                               530                               535                               540
167 Val Lys Glu His Leu Leu Lys Glu Gly Ile Glu Val Arg Leu
168 545                               550                               555
170 <210> SEQ ID NO: 3
171 <211> LENGTH: 587
172 <212> TYPE: DNA
173 <213> ORGANISM: Zea mays
175 <220> FEATURE:
176 <221> NAME/KEY: unsure
177 <222> LOCATION: (495) /
179 <220> FEATURE:
180 <221> NAME/KEY: unsure /
181 <222> LOCATION: (518)
183 <220> FEATURE:
184 <221> NAME/KEY: unsure
185 <222> LOCATION: (577) /
187 <220> FEATURE:
188 <221> NAME/KEY: unsure /
189 <222> LOCATION: (582)
191 <400> SEQUENCE: 3
192 aagaaaaggc ccgctagggc gccgagacag cggaacgttc tctgagtttg agcacgatct 60
193 ccccgggccc cggcgcgcgc gtacgtcccc cttcggcgtc gccagcgcgc tcctggctcc 120

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194 ggctccttca tcgctgctc cagcgtgcct gcgtgacata agcgtcgatt gattggcgag 180
195 aaaggggacg aatgcagccg ccgttgccag gcaggggagc aatggctaac gtcgccgcta 240
196 tcctcaccgt cccctgctcc gcgggcccgc gcccgaggcg gagcaaccag ccccgcgat 300
197 gcggtccgt ctccgtctcc gtctccgtcc gtgcgtcctc cggcgcaaac acggtgactc 360
198 tgctggacta cggcgcgggg aacgtacgca gcgtgcgcaa cgcaattcgc tacctcggt 420
199 tcgacatccg cgacgtgcag agcccggarg acatcgtcgc cggcggaayg ggtcgtcttt 480
200 cccggtgtcg gcgcnttcgg ctccgccatg gacgtccnca ccaggacggg catgccaacg 540
201 cactccgtga gtacatccaa agggaacgcc cttccnagg cnetgcc 587
203 <210> SEQ ID NO: 4
204 <211> LENGTH: 130
205 <212> TYPE: PRT
206 <213> ORGANISM: Zea mays
208 <220> FEATURE:
209 <221> NAME/KEY: UNSURE
210 <222> LOCATION: (90)
212 <220> FEATURE:
213 <221> NAME/KEY: UNSURE
214 <222> LOCATION: (93)
216 <220> FEATURE:
217 <221> NAME/KEY: UNSURE
218 <222> LOCATION: (109)
220 <220> FEATURE:
221 <221> NAME/KEY: UNSURE
222 <222> LOCATION: (115)
224 <220> FEATURE:
225 <221> NAME/KEY: UNSURE
226 <222> LOCATION: (129)
228 <400> SEQUENCE: 4
229 Met Gln Pro Pro Leu Gln Ala Gln Gly Ala Met Ala Asn Val Ala Ala
230 1 5 10 15
232 Ile Leu Thr Val Pro Cys Ser Ala Gly Arg Arg Pro Lys Arg Ser Asn
233 20 25 30
235 Gln Pro Arg Gly Cys Gly Ser Val Ser Val Ser Val Ser Val Arg Ala
236 35 40 45
238 Ser Ser Gly Ala Asn Thr Val Thr Leu Leu Asp Tyr Gly Ala Gly Asn
239 50 55 60
241 Val Arg Ser Val Arg Asn Ala Ile Arg Tyr Leu Gly Phe Asp Ile Arg
242 65 70 75 80
W--> 244 Asp Val Gln Ser Pro Glu Asp Ile Val Xaa Ala Glu Xaa Val Val Phe
245 85 90 95
W--> 247 Pro Gly Val Gly Ala Phe Gly Ser Ala Met Asp Val Xaa Thr Arg Thr
248 100 105 110
W--> 250 Gly Met Xaa Asn Ala Leu Arg Glu Tyr Ile Gln Arg Glu Arg Pro Phe
251 115 120 125
W--> 253 Xaa Gly
254 130
256 <210> SEQ ID NO: 5
257 <211> LENGTH: 1084
258 <212> TYPE: DNA

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Input Set : A:\BB1129 us pct seq lst.txt

Output Set: N:\CRF3\06122002\I831233A.raw

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259 <213> ORGANISM: Zea mays
261 <400> SEQUENCE: 5
262 actagtggta acaaaaggcg atcaatatga tgtaagagat catactagca gcaaagaggt 60
263 aagaaacctt ggcaagccag tcgattttagc aagccagtac tacatagacg gtgctgatga 120
264 ggtcagcttc ttgaatataa ctggtttccg tgactttcca ttgggtgatt tgccaatgct 180
265 agaggtactg cgttgtgcct ctgaaaagggt ttttgtgcca cttacagttg gtgggggcat 240
266 acgagacttc acagatgcaa atggaagata ctactcaagt ttggaggtag catcagaata 300
267 tttcaggtcc ggtgctgaca aaatttcaat tggaagtgat gctgtttatg ctgctgaagc 360
268 ctttttacag actggtgtaa agacagggaa aagcagcttg gagcaaactc ctagagtata 420
269 tggcaatcag gctgtagttg tcagtattga tcctcgacgg gtatatgtca aaagtcaaga 480
270 agatgtgcca tttaaaactg taaaggtgtc cactaaagggt ccatcgggag aagaatatgc 540
271 atggtaccag tgcacagtga atggtggacg tgatagccga gctataggag catatgaact 600
272 agcgaaagct gtggaagaat tgggcgcagg agaaatactt cttaaactgca ttgattgtga 660
273 tggccaagggt tgtggatttg acatagattt ggtaaataat gtttctgatg ctgtgacaat 720
274 coctgtcatt gcgagcagtg gtgctggagc tgttcaacat ttttctgaaa tttttgagaa 780
275 aacaaatgct tctgtgccc ttgctgctgg cattttccac cggaaagagg ttcctatact 840
276 agcagtgaag gagcatctgg tcaatgctgg tgtggaggtc aggggtgaac agggagatcc 900
277 ttcggtttat tgaaatattc ttgtttgatg tcacaactgc tatcagttct gtttctctga 960
278 tgtcgcaact gctatcagat ctgttggtgg cagctggcag tgcataggcc cctgtcgaga 1020
279 actgcagttt ggtaataaat taataatgtg atgcttaaca gattaaaaaa aaaaaaaaaa 1080
280 aaaa 1084
282 <210> SEQ ID NO: 6
283 <211> LENGTH: 295
284 <212> TYPE: PRT
285 <213> ORGANISM: Zea mays
287 <400> SEQUENCE: 6
288 Leu Val Val Thr Lys Gly Asp Gln Tyr Asp Val Arg Asp His Thr Ser
289 1 5 10 15
291 Ser Lys Glu Val Arg Asn Leu Gly Lys Pro Val Asp Leu Ala Ser Gln
292 20 25 30
294 Tyr Tyr Ile Asp Gly Ala Asp Glu Val Ser Phe Leu Asn Ile Thr Gly
295 35 40 45
297 Phe Arg Asp Phe Pro Leu Gly Asp Leu Pro Met Leu Glu Val Leu Arg
298 50 55 60
300 Cys Ala Ser Glu Lys Val Phe Val Pro Leu Thr Val Gly Gly Gly Ile
301 65 70 75 80
303 Arg Asp Phe Thr Asp Ala Asn Gly Arg Tyr Tyr Ser Ser Leu Glu Val
304 85 90 95
306 Ala Ser Glu Tyr Phe Arg Ser Gly Ala Asp Lys Ile Ser Ile Gly Ser
307 100 105 110
309 Asp Ala Val Tyr Ala Ala Glu Ala Phe Leu Gln Thr Gly Val Lys Thr
310 115 120 125
312 Gly Lys Ser Ser Leu Glu Gln Ile Ser Arg Val Tyr Gly Asn Gln Ala
313 130 135 140
315 Val Val Val Ser Ile Asp Pro Arg Arg Val Tyr Val Lys Ser Gln Glu
316 145 150 155 160
318 Asp Val Pro Phe Lys Thr Val Lys Val Ser Thr Lys Gly Pro Ser Gly
319 165 170 175
321 Glu Glu Tyr Ala Trp Tyr Gln Cys Thr Val Asn Gly Gly Arg Asp Ser

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 06/12/2002
PATENT APPLICATION: US/09/831,233A TIME: 14:14:11

Input Set : A:\BB1129 us pct seq lst.txt
Output Set: N:\CRF3\06122002\I831233A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 495,518,577,582
Seq#:4; Xaa Pos. 90,93,109,115,129
Seq#:7; N Pos. 6,12,43,56,60,154,155,161,163,166,202,215,266,271,274,275
Seq#:7; N Pos. 277,306,320,346,347,356,393,434,441,456,466,474
Seq#:8; Xaa Pos. 23,25,26,27,39,43,60,62,63,64,74,78
Seq#:9; N Pos. 125,266,315,366,405,441,443,445,453,458,461,475,480,492,494
Seq#:10; Xaa Pos. 72
Seq#:13; N Pos. 276
Seq#:14; Xaa Pos. 92